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=> d his

     (FILE 'HOME' ENTERED AT 12:38:11 ON 10 JAN 2009)

     FILE 'BIOSIS, MEDLINE, CAPLUS, WPIDS, USPATFULL' ENTERED AT 12:38:53 ON
     10 JAN 2009
L1         33167 S SOLID PHASE AND SURFACE AND OLIGONUCLEOTIDE
L2          1055 S L1 AND 3(2A)OVERHANG
L3             1 S L2 AND SURFACE (3A)OLIGONUCLEOTIDE (4A) COVALENT
L4          1172 S L1 AND 3 (5A) OVERHANG
L5             7 S L4 AND SURFACE (4A) OLIGONUCLEOTIDE (4A) COVALENT
L6             7 S L5 NOT L3\
L7             6 S L5 NOT L3

=> s l7 and liga?
L8             6 L7 AND LIGA?

=> s l8 and ligase
L9             6 L8 AND LIGASE

=> d l9 bib abs 1-6

L9   ANSWER 1 OF 6  USPATFULL on STN
AN     2006:80401  USPATFULL
TI     Method of producing a DNA library using positional amplification
IN     Langmore, John P., Ann Arbor, MI, UNITED STATES
       Makarov, Vladimir L., Ann Arbor, MI, UNITED STATES
PI     US 20060068394      A1  20060330
AI     US 2004-798025      A1  20040311 (10)
RLI    Division of Ser. No. US 2001-860738, filed on 18 May 2001, GRANTED, Pat.
       No. US 6828098
PRAI   US 2000-206095P     20000520 (60)
DT     Utility
FS     APPLICATION
LREP   FULBRIGHT & JAWORSKI, LLP, 1301 MCKINNEY, SUITE 5100, HOUSTON, TX,
       77010-3095, US
CLMN   Number of Claims: 13
ECL    Exemplary Claim: 1-189
DRWN   114 Drawing Page(s)
LN.CNT 9395
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB     The disclosed invention relates to general and specific methods to use
       the Primer Extension/Nick Translation (PENT) reaction to create an
       amplifiable DNA strand, called a PENTAmer. A PENTAmers can be made for
       the purpose of amplifying a controlled length of DNA located at a
       controlled position within a DNA molecule, a process referred to as
       Positional Amplification by Nick Translation (PANT). In contrast to PCR,
       which amplifies DNA between two specific sequences, PANT can amplify DNA
       between two specific positions. PENTAmers can be created to amplify-very
       large regions of DNA (up to 500,000 bp) as random mixtures (unordered
       positional libraries), or as molecules sorted according to position
       (ordered positional libraries). PANT is fast and economical, because
       PENTAmer preparation can be multiplexed. A single PENTAmer preparation
       can include very complex mixtures of DNA such as hundreds of
       large-insert clones, complete genomes, or cDNA libraries. Subsequent PCR
       amplification of the preparation using a single specific primer can
       positionally amplify contiguous regions along a specific clone, along a
       specific genomic region, or along a specific expressed sequence.
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CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L9 ANSWER 2 OF 6 USPATFULL on STN
AN 2005:220911 USPATFULL
TI Nucleic acid analysis techniques
IN Lockhart, David J., Mountain View, CA, UNITED STATES
Chee, Mark, Palo Alto, CA, UNITED STATES
Gunderson, Kevin, Santa Clara, CA, UNITED STATES
Chaoqiang, Lai, Sunnyvale, CA, UNITED STATES
Wodicka, Lisa, Santa Clara, CA, UNITED STATES
Cronin, Maureen T., Los Altos, CA, UNITED STATES
Lee, Danny, RTP, NC, UNITED STATES
Tran, Huu M., Milpitas, CA, UNITED STATES
Matsuzaki, Hajime, Palo Alto, CA, UNITED STATES
McGall, Glenn H., Mountain View, CA, UNITED STATES
Barone, Anthony D., San Jose, CA, UNITED STATES
PA Affymetrix, Inc., Santa Clara, CA, UNITED STATES (U.S. corporation)
PI US 20050191646 A1 20050901
AI US 2004-961341 A1 20041007 (10)
RLI Continuation of Ser. No. US 2001-880727, filed on 13 Jun 2001, GRANTED, Pat. No. US 6858711 Continuation of Ser. No. US 1997-882649, filed on 25 Jun 1997, GRANTED, Pat. No. US 6344316 Continuation of Ser. No. WO 1997-US1603, filed on 22 Jan 1997, PENDING
PRAI US 1996-10471P 19960123 (60)
US 1997-35170P 19970109 (60)
DT Utility
FS APPLICATION
LREP TOWNSEND AND TOWNSEND AND CREW LLP, TWO EMBARCADERO CENTER, 8TH FLOOR, SAN FRANCISCO, CA, 94111-3834, US
CLMN Number of Claims: 49
ECL Exemplary Claim: 1
DRWN 47 Drawing Page(s)
LN.CNT 6358
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides a simplified method for identifying differences in nucleic acid abundances (e.g., expression levels) between two or more samples. The methods involve providing an array containing a large number (e.g. greater than 1,000) of arbitrarily selected different oligonucleotide probes where the sequence and location of each different probe is known. Nucleic acid samples (e.g. mRNA) from two or more samples are hybridized to the probe arrays and the pattern of hybridization is detected. Differences in the hybridization patterns between the samples indicates differences in expression of various genes between those samples. This invention also provides a method of end-labeling a nucleic acid. In one embodiment, the method involves providing a nucleic acid, providing a labeled oligonucleotide and then enzymatically ligating the oligonucleotide to the nucleic acid. Thus, for example, where the nucleic acid is an RNA, a labeled oligoribonucleotide can be ligated using an RNA ligase. In another embodiment, the end labeling can be accomplished by providing a nucleic acid, providing labeled nucleoside triphosphates, and attaching the nucleoside triphosphates to the nucleic acid using a terminal transferase.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L9 ANSWER 3 OF 6 USPATFULL on STN
AN 2005:183385 USPATFULL
TI Nucleic acid analysis techniques
IN Lockhart, David J., Mountain View, CA, UNITED STATES
Chee, Mark, Palo Alto, CA, UNITED STATES

Gunderson, Kevin, Santa Clara, CA, UNITED STATES
Chaoqiang, Lai, Sunnyvale, CA, UNITED STATES
Wodicka, Lisa, Santa Clara, CA, UNITED STATES
Cronin, Maureen T., Los Altos, CA, UNITED STATES
Lee, Danny H., RTP, NC, UNITED STATES
Tran, Huu M., Milpitas, CA, UNITED STATES
Matsuzaki, Hajime, Palo Alto, CA, UNITED STATES
McGall, Glenn H., Palo Alto, CA, UNITED STATES
Barone, Anthony D., San Jose, CA, UNITED STATES

PA Affymetrix, INC., Santa Clara, CA, UNITED STATES (U.S. corporation)

PI US 20050158772 A1 20050721

AI US 2004-213667 A1 20041223 (11)

RLI Continuation of Ser. No. US 2001-880727, filed on 13 Jun 2001, GRANTED, Pat. No. US 6858711 Continuation-in-part of Ser. No. US 1997-882649, filed on 25 Jun 1997, GRANTED, Pat. No. US 6344316 Continuation of Ser. No. WO 1997-US1603, filed on 22 Jan 1997, PENDING

PRAI US 1996-10471P 19960123 (60)
US 1997-35170P 19970109 (60)

DT Utility

FS APPLICATION

LREP AFFYMETRIX, INC, ATTN: CHIEF IP COUNSEL, LEGAL DEPT., 3380 CENTRAL EXPRESSWAY, SANTA CLARA, CA, 95051, US

CLMN Number of Claims: 37

ECL Exemplary Claim: 1

DRWN 47 Drawing Page(s)

LN.CNT 6328

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention provides a simplified method for identifying differences in nucleic acid abundances (e.g., expression levels) between two or more samples. The methods involve providing an array containing a large number (e.g. greater than 1,000) of arbitrarily selected different oligonucleotide probes where the sequence and location of each different probe is known. Nucleic acid samples (e.g. mRNA) from two or more samples are hybridized to the probe arrays and the pattern of hybridization is detected. Differences in the hybridization patterns between the samples indicates differences in expression of various genes between those samples. This invention also provides a method of end-labeling a nucleic acid. In one embodiment, the method involves providing a nucleic acid, providing a labeled oligonucleotide and then enzymatically ligating the oligonucleotide to the nucleic acid. Thus, for example, where the nucleic acid is an RNA, a labeled oligoribonucleotide can be ligated using an RNA ligase. In another embodiment, the end labeling can be accomplished by providing a nucleic acid, providing labeled nucleoside triphosphates, and attaching the nucleoside triphosphates to the nucleic acid using a terminal transferase.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L9 ANSWER 4 OF 6 USPATFULL on STN

AN 2003:93005 USPATFULL

TI Nucleic acid analysis techniques

IN Lockhart, David J., Santa Clara, CA, UNITED STATES
Chee, Mark, Palo Alto, CA, UNITED STATES
Gunderson, Kevin, Palo Alto, CA, UNITED STATES
Lai, Chaoqiang, Santa Clara, CA, UNITED STATES
Wodicka, Lisa, Santa Clara, CA, UNITED STATES
Cronin, Maureen T., Los Altos, CA, UNITED STATES
Lee, Danny H., San Jose, CA, UNITED STATES
Tran, Huu M., San Jose, CA, UNITED STATES
Matsuzaki, Hajime, Palo Alto, CA, UNITED STATES

McGall, Glenn H., Mt. View, CA, UNITED STATES
Barone, Anthony D., San Jose, CA, UNITED STATES
PI US 20030064364 A1 20030403
US 6858711 B2 20050222
AI US 2002-880727 A1 20020411 (9)
RLI Continuation of Ser. No. US 1997-882649, filed on 25 Jun 1997, GRANTED, Pat. No. US 6344316 Continuation of Ser. No. WO 1997-US1603, filed on 22 Jan 1997, UNKNOWN
PRAI US 1996-10471P 19960123 (60)
US 1997-35170P 19970109 (60)
DT Utility
FS APPLICATION
LREP TOWNSEND AND TOWNSEND AND CREW, LLP, TWO EMBARCADERO CENTER, EIGHTH FLOOR, SAN FRANCISCO, CA, 94111-3834
CLMN Number of Claims: 49
ECL Exemplary Claim: 1
DRWN 47 Drawing Page(s)
LN.CNT 6539
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides a simplified method for identifying differences in nucleic acid abundances (e.g., expression levels) between two or more samples. The methods involve providing an array containing a large number (e.g. greater than 1,000) of arbitrarily selected different oligonucleotide probes where the sequence and location of each different probe is known. Nucleic acid samples (e.g. mRNA) from two or more samples are hybridized to the probe arrays and the pattern of hybridization is detected. Differences in the hybridization patterns between the samples indicates differences in expression of various genes between those samples. This invention also provides a method of end-labeling a nucleic acid. In one embodiment, the method involves providing a nucleic acid, providing a labeled oligonucleotide and then enzymatically ligating the oligonucleotide to the nucleic acid. Thus, for example, where the nucleic acid is an RNA, a labeled oligoribonucleotide can be ligated using an RNA ligase. In another embodiment, the end labeling can be accomplished by providing a nucleic acid, providing labeled nucleoside triphosphates, and attaching the nucleoside triphosphates to the nucleic acid using a terminal transferase.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L9 ANSWER 5 OF 6 USPATFULL on STN
AN 2003:58052 USPATFULL
TI Method of producing a DNA library using positional amplification
IN Langmore, John P., Ann Arbor, MI, UNITED STATES
Makarov, Vladimir L., Ann Arbor, MI, UNITED STATES
PI US 20030040620 A1 20030227
US 6828098 B2 20041207
AI US 2001-860738 A1 20010518 (9)
PRAI US 2000-206095P 20000520 (60)
DT Utility
FS APPLICATION
LREP FULBRIGHT & JAWORSKI, LLP, 1301 MCKINNEY, SUITE 5100, HOUSTON, TX, 77010-3095
CLMN Number of Claims: 272
ECL Exemplary Claim: 1
DRWN 114 Drawing Page(s)
LN.CNT 9894
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The disclosed invention relates to general and specific methods to use the Primer Extension/Nick Translation (PENT) reaction to create an

amplifiable DNA strand, called a PENTAmer. A PENTAmers can be made for the purpose of amplifying a controlled length of DNA located at a controlled position within a DNA molecule, a process referred to as Positional Amplification by Nick Translation (PANT). In contrast to PCR, which amplifies DNA between two specific sequences, PANT can amplify DNA between two specific positions. PENTAmers can be created to amplify very large regions of DNA (up to 500,000 bp) as random mixtures (unordered positional libraries), or as molecules sorted according to position (ordered positional libraries). PANT is fast and economical, because PENTAmer preparation can be multiplexed. A single PENTAmer preparation can include very complex mixtures of DNA such as hundreds of large-insert clones, complete genomes, or cDNA libraries. Subsequent PCR amplification of the preparation using a single specific primer can positionally amplify contiguous regions along a specific clone, along a specific genomic region, or along a specific expressed sequence.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L9 ANSWER 6 OF 6 USPATFULL on STN
AN 2002:24160 USPATFULL
TI Nucleic acid analysis techniques
IN Lockhart, David J., Santa Clara, CA, United States
Chee, Mark, Palo Alto, CA, United States
Gunderson, Kevin, Palo Alto, CA, United States
Chaoqiang, Lai, Santa Clara, CA, United States
Wodicka, Lisa, Santa Clara, CA, United States
Cronin, Maureen T., Los Altos, CA, United States
Lee, Danny, San Jose, CA, United States
Tran, Huu M., San Jose, CA, United States
Matsuzaki, Hajime, Palo Alto, CA, United States
PA Affymetrix, Inc., Santa Clara, CA, United States (U.S. corporation)
PI US 6344316 B1 20020205
AI US 1997-882649 19970625 (8)
RLI Continuation of Ser. No. WO 1997-US1603, filed on 22 Jan 1997
PRAI US 1997-35170P 19970109 (60)
US 1996-10471P 19960123 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Houtteman, Scott W.
LREP Townsend and Townsend and Crew LLP
CLMN Number of Claims: 28
ECL Exemplary Claim: 1
DRWN 54 Drawing Figure(s); 47 Drawing Page(s)
LN.CNT 6540
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides a simplified method for identifying differences in nucleic acid abundances (e.g., expression levels) between two or more samples. The methods involve providing an array containing a large number (e.g. greater than 1,000) of arbitrarily selected different oligonucleotide probes where the sequence and location of each different probe is known. Nucleic acid samples (e.g. mRNA) from two or more samples are hybridized to the probe arrays and the pattern of hybridization is detected. Differences in the hybridization patterns between the samples indicates differences in expression of various genes between those samples. This invention also provides a method of end-labeling a nucleic acid. In one embodiment, the method involves providing a nucleic acid, providing a labeled oligonucleotide and then enzymatically ligating the oligonucleotide to the nucleic acid. Thus, for example, where the nucleic acid is an RNA, a labeled oligoribonucleotide can be ligated using an RNA ligase. In another embodiment, the end labeling can be

accomplished by providing a nucleic acid, providing labeled nucleoside triphosphates, and attaching the nucleoside triphosphates to the nucleic acid using a terminal transferase.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.